Compositions for diagnosis and therapy of diseases associated with aberrant expression of Futrins (R-Spondins)

The present invention relates to compositions useful for the diagnosis and therapy of diseases associated with aberrant expression of the genes encoding the proteins Futrin 1, 2, 3 and/or 4 (= R-Spondin 2, 3, 1 and 4, respectively). These diseases include tumors of e.g. the breast, ovary, liver, uterus, cervix, colon, lung, ovary, rectum, testis, pancreas, bones and skin, as well as diseases involving muscle, bone, lipid and glucose metabolism, and obesity. The present invention also relates to a pharmaceutical composition containing a compound which is capable of modifying (a) the expression of the gene encoding Futrin 1, 2, 3 and/or 4 or (b) the activity of Futrin 1, 2, 3 and/or 4.

The Wnt signal cascade plays a crucial role as regards regulation of survival, proliferation and differentiation of cells during embryogenesis, and in the adult as shown, e.g., in *Drosophila, Xenopus* and mice (Nusse and Varmus, Cell <u>69</u> (1992), 1073-1087). Wnt-genes encode secretory glycoproteins which activate a well characterized signal cascade via a Wnt receptor called „frizzled„.

The Wnt signalling cascade and its components also play an important role in various diseases which makes it desirable to modulate its activity:

i) Cancer
Tumorigenesis represents a complex multistage process in which genetic changes and environmental factors are thought to deregulate the cellular processes that control cell proliferation and differentiation. Several studies indicate that an aberrant Wnt signal cascade is involved in the development of colon cancer, breast cancer and melanoma

(Pfeifer, Science, 275 (1997), 1752-1753; Polakis, Genes Dev. 14 (2000), 1837-1851). The first gene encoding a protein of the Wnt signal cascade, *int-1*, was isolated from mouse mammary tumor virus (MMTV) and it could be shown that it is an oncogene. It is thus well established that an aberrant regulation of the activity of Wnt and/or components of the Wnt signal cascade downstream of the Wnt signal, e.g., beta-catenin and APC, are involved in tumorigenesis.

ii) Bone disease

Wnt signals promote bone formation (e.g. Yang, Development, 130(2003), 1003-15; Fischer, J.Biol.Chem. 277 (2002) 30870-30878). Consistent with this notion, a gain-of-function mutation of the Wnt receptor LRP5 causes high bone disease (Boyden, et al., 346 (2002) N Engl J Med, 1513-21.; Little, et al., 70 (2002) Am J Hum Genet, 11-9.). Conversely, inactivating mutations in LRP5 leads to osteoporosis-pseudoglioma syndrome in humans (Kato, et al., 157 (2002) J Cell Biol, 303-14.; Gong, et al., 107 (2001) Cell, 513-23.).

iii) Eye disease

Inactivating mutation in the Wnt receptor LRP5 lead to pseudoglioma in humans and eye malformations in mice (Kato, et al., 157 (2002) J Cell Biol 303-314; Gong, et al., 107 (2001) Cell, 513-523).

iv) Kidney

Aberrant Wnt signalling is involved in renal fibrosis (Surendran, Am J Physiol Renal Physiol 282 (2002) 431-441) and polycystic kidney disease (Saadi-Kheddouci, Oncogene 20 (2001) 5972-5981).

v) Lipid and glucose metabolism, obesity

Deficiency of the Wnt receptor LRP5 in mice leads to increased plasma cholesterol levels in mice fed a high-fat diet, because of the decreased hepatic clearance of chylomicron remnants. In

addition, when fed a normal diet, LRP5-deficient mice show a markedly impaired glucose tolerance (Fujino, et al., 100 (2003) Proc Natl Acad Sci U S A, 229-234.) Administration of the LRP5 antagonist Dkk1 to mice reduces glucose uptake in various cell line and decreases fat deposition (WO 02/066509).

It is thus clear from the above that the Wnt signalling pathway is involved in a variety of human diseases. Yet, means for the therapy or diagnosis of diseases associated with a dis-regulated Wnt signal cascade are insufficiently available. Thus, the use of reliable diagnostic molecular markers would be helpful for an understanding of the molecular basis of diseases associated with an aberrant Wnt signal cascade. It can be expected that such markers are also useful for therapy and for the development of novel therapeutic avenues for treatment of Wnt signal cascade dependent diseases, as detailed above.

Thus, the technical problem underlying the present invention is to provide means for diagnosis and therapy of diseases associated with an aberrant Wnt signal cascade.

The solution to said technical problem is achieved by providing the embodiments characterized in the claims.

During the experiments resulting in the present invention four genes, *futrin 1, 2, 3* and *4,* could be identified the products of which are modulators of the Wnt pathway. Futrin 2 was previously identified as hPWTSR (Chen et al., 29 (2002), Mol. Biol. Rep. 287-292), a protein of before unknown role or function, expressed in numerous cell types. Further, human Futrin 1, 2, 3, and 4 were described as Stem Cell Growth Factor-Like Polypeptides, which are able to promote proliferation of hematopoietic stem cells (WO-A-01/77169 ; WO-A-01/07611).

In the present invention the following is shown for the first time: 1) Futrins enhance Wnt signalling and this is of physiological relevance since inhibition of Futrin 1 or 2 results in inhibition of the Wnt signal cascade (Wnt/ß-catenin signalling). These data show that Futrins can be regarded as Wnt modulators. Futrin 1 (Rspo2) is coexpressed with and positively regulated by Wnt signals and synergizes with Wnt to activate ß-catenin. Analysis of functional interaction with components of the Wnt/ß-catenin pathway suggests that Rspo2 functions extracellularly at the level of receptor ligand interaction. Antisense Morpholino experiments in *Xenopus* embryos and RNAi experiments in HeLa cells revealed that *Rspo2* is required for Wnt/ß-catenin signalling. *In Xenopus* embryos depleted of Rspo2 the muscle markers myoD and myf5 fail to be activated and later muscle development is impaired. The results indicate that *Rspo2* is a novel activator of the Wnt/ß-catenin cascade. Thus, Futrins like Rspo2 (Futrin 1) are useful for the diagnosis and the development of therapies for Wnt-LRP mediated diseases, including but not limited to tumor suppression, bone formation, cholesterol and glucose metabolism (including diabetes), obesity, kidney disease and eye disease. 2.) Since the data obtained show that Futrin 1 is required for muscle formation Futrin 1 is useful for the diagnosis and the development of therapies for muscle related diseases, including muscle regeneration. 3.) The data show that Futrins are aberrantly expressed in a variety of human tumors. Thus, Futrins are useful for tumor diagnosis and the development of cancer therapies. For example it has been found out that in most of the tumors the expression of Futrins 1-3 is dramatically decreased (colon, stomach, lung, rectum tumors for Futrin 1, breast, ovary, bladder, uterus, cervix, rectum tumors for Futrin 2, uterus and cervix tumors for Futrin 3). In a few cases the expression of Futrin 1-3 is upregulated (one case of stomach tumor for Futrin 1 and 2, ovary tumor for Futrin 3). Futrin 4 shows very low level of expression in most

of the tissues studied, except ovary.

Thus, the inhibition of the Wnt signal cascade by inhibiting the expression/activity of Futrins or by stimulating the expression/activity of the Futrins will have a therapeutic effect. Likewise, the activation of the Wnt signal cascade by decreasing the expression of Futrin and/or by repressing the activity of the polypeptide itself will have a therapeutic effect.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: Identification of Xenopus Futrin 1 (Rspo2)
TOP-FLASH reporter, vector DNA from pools of 250 clones each and pCSfrizzled8 were co-transfected. Luciferase reporter assays in 293T cells were carried out in 96 well plates in duplicates as described (Wu et al., Curr Biol 10 (2000), 1611-1614). Luciferase activity was normalized against cotransfected Renilla-luc activity using a commercial kit (Clonetech). RLU: relative luciferase units

Figure 2: Futrin 1 (Rspo2) promotes Wnt/ß-catenin signalling
(A) Identification of Xenopus Rspo2 by expression screening. An expression screen was carried out in 293T cells transfected with a Wnt-responsive reporter (TOPFLASH) and plasmid DNA pools from a Xenopus eye cDNA library. RLU: relative light units.
(B) The C-terminus of Rspo2 mediates cell surface retention. Myc-tagged Rspo2 (wt) or Rspo2ΔC (ΔC) were transfected in 293T cells, and cell lysate and medium were analysed by Western blot. Co, untransfected cells.
(C) Rspo2 activates Wnt/ß-catenin signalling. TOPFLASH luciferase reporter assays were carried out in 293T cells with the following transfected DNAs: mouse Wnt1 (Wnt), 5 ng; mouse frizzled8 (fz), 1 ng; Xenopus Rspo2 (Rspo2), 0.1, 0.3,

0.9 and 2.7 ng.

(D) Rspo2 enhances Wnt3a signalling. Mouse Wnt3a, *Xenopus* Rspo2ΔC (Rspo2ΔC) or mock-conditioned media were added to 293T cells followed by TOPFLASH luciferase reporter assays. **(E)** Rspo2 stabilizes ß-catenin. (top) 293T cells were treated with Rspo2ΔC, Wnt3a or mock-conditioned media for 1 or 4 hours as indicated. Cytosolic fractions were subjected to Western blot and probed for ß-catenin and α-tubulin (loading control). (bottom) immunohistochemical staining of ß-catenin in SHEP cells after 3 hour treatment with the conditioned media indicated. Arrowheads indicate nuclear ß-catenin. The percentage of cells showing the represented staining is 90% (Co), 85% (Rspo2), 80% (Wnt3a) and 90% (Wnt3a + Rspo2). **(F)** Domain analysis of Rspo2. (top) schematic drawing of *Xenopus* Rspo2 and deletion constructs. sp, signal peptide; FU1, 2, furin-like domains; TSP1, thrombospondin type 1 domain; C, positively charged C-terminus. (bottom). TOPFLASH luciferase reporter assays were carried out in 293T cells with the indieated constructs. Equal protein production was confirmed by Western blot (data not shown).

Figure 3: Multisequence nucleic acid alignment of cDNAs encoding human Futrin 1,2 3 and 4 and Xenopus Futrin 1
Identical nucleotides are highlighted in black. All nucleic acid sequences begin with the translation initiator ATG codon indicated with an asterisk.

Figure 4: Multisequence amino acid alignment of human Futrin 1,2 3 and 4 deduced from human cDNAs (see Figure 3)
Identical amino acids are highlighted in black, similar amino acids are in grey.

Figure 5: Futrins promote Wnt signalling
Cotransfection experiments in 293T cells. Wnt-responsive luciferase reporter assays were performed in 96 well plates in triplicates as described (Wu et al., Curr Biol 10 (2000),

1611-1614). Luciferase activity was normalized against Renilla activity using a commercial kit (Clonetech). Wnt1 = mouse Wnt1, fz8 = mouse frizzled8, Futrin1 = *xenopus* Futrin 1, Wnt3A = mouse Wnt3A, (0.1ng) in A indicates amount of plasmid DNA transfected per well, RLU: relative luciferase units

Figure 6: Sequence comparison of human Rspo proteins (hR-spondin 1 to 4)

(A) Alignment of human (h) Rspo proteins (corresponding to the alignments of human Fut1-4 in Figure 4 except that different designations are used). The signal peptide, furin-like domains and thrombospondin type 1 domain are underlined and conserved amino acids are shown in black. **(B, C)** Rspo homology matrix showing overview of amino acid identity in % between human Rspo proteins **(B)** and between *Xenopus (X)* or mouse (m) Rspo2 and human Rspo proteins, respectively **(C)**.

Figure 7: Human Futrin 1 and 2 are required for Wnt signalling
Hela cells were transfected in 24-well plates with the Wnt reporter 7LEF-Rev-fosLuc, pRL-TK and pSuper plasmids that produce either siRNA against human Futrin1 and 2 or a nonsense control. Three days after transfection, mouse Wnt3A conditioned medium was added to the culture to stimulate Wnt signalling. 24 hours later, luciferase activity was determined.

Figure 8: Expression analysis of *Xenopus* and mouse *R-spondins*
(A) Rspo2 expression during *Xenopus* development at the indieated embryonic stages analysed by RT-PCR. Histone H4 was used for normalization. -RT, minus reverse transcription control.
(B-H) *Xenopus* whole mount in situ hybridizations of the indicated genes. **(B)** Stage 11 embryo, dorso-vegetal view; dbl, dorsal blastoporal lip. **(C)** Stage 12 embryo, dorsal view with anterior up. An anterior neural expression domain is

indicated by arrowhead. **(D)** Stage 15 embryo, dorsal view with anterior up. **(E)** Stage 14 embryo, dorsal view with anterior up. **(F-G)** Tailbud stage embryos; ba, branchial arches; cm, cranial musculature; di, diencephalon; dnt, dorsal neural tube; mhb, midbrain-hindbrain boundary; ov, otic vesicle; pn, pronephros; pdm, proctodeum; s, somites; tb, tailbud mesoderm. Inset in (F) shows a transverse section at the level indicated by arrowhead, showing expression in dorsal neural tube and in the dorsal- and ventral-most parts of the somites. **(H)** Dissected *Xenopus* tadpole brain (lateral view) showing expression in diencephalons (di) and zona limitans intrathalamica (zli), where *sonic hedgehog* is expressed (inset). dt, vt, dorsal and ventral thalamus, respectively, sc, spinal cord; tel, telencephalon; **(I-M)** Mouse whole mount in situ hybridizations of the indicated genes. **(I)** limb buds of day 12.5 mouse embryos. AER, apical ectodermal ridge. **(J)** Day 7.5 mouse embryo showing *Rspo3* expression in the primitive streak. **(K-M)** Day 9.5 mouse embryos. di, diencephalon; dnt, dorsal neural tube; inet, metencephalon; tel, telencephalon.

Figure 9:   Regulation   of   *Xenopus   R-spondins   by*   Wnt signalling

(A) Comparison of *XRspo2, XWnt8* and *XWnt3a* expression pattern in early neurula embryos by whole mount in situ hybridization. Dorsal view, anterior up.

(B) (top) Diagram of experiment. Four cell stage embryos were injected with 50 pg pCS-ppl (preprolactin), pCS*XWnt8* or *pCS-β-catenin* into each blastomere, DMZs were dissected, cultured until stage 11 equivalent and analyzed by RT-PCR. (Bottom) RT-PCR analysis of the indicated genes. -RT, minus reverse transcription control.

(C-E) Four cell stage embryos were injected with 50 pg *pCS-Wnt8, pCS-Wizt3a* or pCS-*ppl* into one blastomere and fixed at stage 11 for in situ hybridisation with *XRspo2*.

Figure 10: Futrin 2 is required for muscle formation

A. Depletion of Futrin 1 protein causes downregulation of early muscle markers and muscle defects.(A,C,E,G,I,K) Embryos injected with control morpholino oligo (5ng), with Fut1-Mo (5ng). Oligos were mixed with lineage tracer mRNA (LacZ) (blue staining)in (C,D,E,F,G,H) or preprolactin (ppl) RNA, visualised by *in situ* hybridisation (red staining)(A,B,J,K,L). In situ hybridization with probes to Xmyf5 (A,B), XmyoD (C,D), Xbra (E,F), Xnot (G,H) and muscle actin (I-L) (magenta staining). Embryos in K and L are cut transversally. Note reduction of muscle in L (right side).

B. Fut1-Mo act specifically to inhibit translation of their cognate DNA constructs when overexpressed in embryos. mRNA (C-terminal myc tagged fut1) was injected equatorially in both blastomeres at 2-cell stage embryos. The same embryos were then injected at the 8-cell stage with 5ng of Fut1-Mo (lane3) or control morpholino (lane2) in all vegetal blastomeres and harvested at stage 11. Tagged. Futrin1 protein was then visualised with a-myc anibody.

C. Rescue of muscle marker reduction caused by Fut1-Mo by coinjection of XFut1 mRNA containing point mutations in the 5'region corresponding to morpholino oligo. Embryos were coinjected with 5 ng of Fut1-Mo (1,2) with 50 pg of ppl or XFut1 mRNA radially in one blastomere at 4-cell stage.

Expression of MyoD (1,3) and Myf5 (2,4) were analysed by in situ hybridization. All embryos were grouped into 3 classes (examples for MyoD are shown on the bottom of the figure): embryos with expression level on the injected side from 1-30%(class A); 30-70%(class B), and 70-100%(class C) from normal level. Bars represent the percentage of the embryos corresponding to type A,B or C. (n for Fut-Mo + ppl: 57 embryos for MyoD, 45 embryos for Myf5; n for Fut-Mo + mRNA Ffut1: 39 embryos for MyoD and 41 embryo for Myf5).

<u>Figure 11: Rspo2 promotes neural and muscle differentiation</u>
<u>in *Xenopus*</u>

(A) Four-cell stage embryos were injected animally with 100 pg *Rspo2, 100* pg *Xwnt8,* or 200 *pg β-catenin* mRNA in each blastomere. At stage 8, animal caps were dissected, cultured until stage 18 equivalent and analyzed for expression of the indicated marker genes, -RT, minus reverse transcription control.

(B) Two-cell stage embryos were injected with 100 pg *Rspo2* or *preprolactin (ppl)* mRNA in each blastomere. Note ectopic cement glands (arrowhead) and shortened body axis in *Rspo2* injected embryo.

(C-J) Whole mount in situ hybridisations of the indicated genes. Eight-cell stage embryos were injected with 100 pg of *Rspo2* or *ppl* mRNAs as indicated into one animal blastomere. LacZ mRNA was coinjected as lineage tracer in all panels except C, G and H.

(C-H) Stage 15 neurulae in anterior view.

(I-J) Stage 11 gastrulae in vegetal view, dorsal up.

(K-N) *Rspo2* promotes muscle formation. **(K)** Diagram of the experiments. Four-cell stage embryos were injected with 50 pg plasmid DNA constructs in all blastomeres, the indicated fragments were explanted at stage 10.5, cultured, and processed for whole mount in situ hybridisation **(M)** of RT-PCR **(N)**.

(L) Stage 40 equivalent VMZ of LMZ explants. Note tail-like structures in VMZs from *Rspo2* injected embryos.

(M) *In situ* hybridization of stage 25 VMZs for *muscle actin*.

(N) RT-PCR analysis for the indicated genes in stage 25 equivalent VMZ and stage 11 equivalent DMZ explants. Xdd 1, dominant negative. *Xenopus dishevelled,; Co, preprolactin.*

<u>Figure 12: Rspo2 interferes with BMP-4, Activin and Nodal but</u>
<u>not with FGF in *Xenopus*</u>

(A-D) Four-cell stage embryos were injected animally with indicated RNAs. At stage 8, animal caps were dissected, cultured until stage 10 equivalent and analyzed for expression of *Vent2* **(A)** or *Xbra* **(B-D)**. -RT, minus reverse transcription control. Embryos injected with *100 pg preprolactin* (ppl) were used as control. Amounts of mRNAs used : 100 pg Rspo2, 50 pg or 250 pg of *BMP-4,* 50 pg of *activin, 25* or 100 pg of *Wnt8,* 200 pg of *ß-catenin,* 50 or 100 pg of *Xnrl, 2* or *20* pg of *FGF8.*

Figure *13: Xenopus Rspo2* is required for muscle formation

(A) Rspo2Mo specifically inhibits translation of its cognate DNA. Top, Diagram of the experiment. Two-cell stage *Xenopus* embryos were injected with 100 pg Myc-tagged Rspo2 mRNA in the animal region, at 8-cell stage, the same embryos were then injected with 5ng of Rspo2Mo of CoMo in all animal blastomeres, harvested at stage 11 and processed for Western blot analysis of Myc-tagged Rspo2 and α-tubulin.

(B) Depletion of Rspo2 protein causes muscle defects and down-regulation of myogeneic markers. Four-cell stage embryos were injected equatorially into one blastomere with 5 ng control morpholino oligonucleotides (CoMo) or Rspo2Mo as indicated together with 50 pg *ppl* mRNA or 50 pg *LacZ* RNA as lineage tracer and analysed at tailbud of gastrula stage by in situ hybridization for the indicated genes. In (a-f) double in situ hybridization for gene of interest (dark blue) and for ppl (red) was used. (a-d) Stage 25 embryos. (a-b): myotomes, visualised by *muscle actin* expression show malformations an Rspo2Mo injected side (b). (c-d) Transversal section at the trunk level showing reduced muscle volume in (d). (e-h): *myf5* and *myoD* expression (dark blue) is down-regulated in the Rspo2Mo injected region (red in e,f of light blue in g,h). (i-l): *Xbra* and *Xnot2* expression (dark blue) is not affected in the region of Rspo2Mo injections (light blue).

(C) Rspo2Mo acts specifically. Rescue of *myf5* reduction by co-injected *Rspo2* mRNA. Four cell stage embryos were injected in one blastomere with 5ng of control morpholino (CoMo), Rspo2Mo, 50pg *ppl* mRNA of 50 pg *Rspo2* mRNA containing mismatches to Rspo2Mo. Expression of *myf5* was analysed by in situ hybridization at gastrula stage. The percentage of embryos with strongly affected (A), moderately reduced (B) and normal myf5 expression (C) as displayed in the representative embryos is indicated. Standard deviation was calculated from three independent experiments.

(D) Rspo2Mo Blocks Wnt signalling upstream of *dishevelled* during muscle formation. Four-cell stage embryos were radially injected with 5ng of Rspo2Mo or CoMo, 50pg *pCS-XWnt8, pCS-dishevelled* (Xdsh), pCS-dominant negative *GSK-3ß* (dnGSK) or *pCS-ß-catenin*. At stage 10.5 DMZs (a) or VMZs (b) or LMZs (c-d) were explanted and cultured until stage 11 (a,c) or 25 (b ,d) for RT-PCR analysis of the genes indicated. -RT: minus reverse transcription control.

Figure 14: *R-spondins* are required for Wnt signalling in HeLa cells

(A) RT-PCR analysis showing differential expression of *human Rspo1-4* in HeLa and 293T cell lines. *Actin* was used for normalisation.

(B) Specificity of siRNAs. 293T cells were cotransfected with pSUPER-Rspo2 or -3 (siRNA), FLAG-tagged Rspo3 and GFP (transfection control). Expression of Rspo3 and GFP were analyzed by Western blot.

(C-D) R-spondins are required for Wnt/ß-catenin signalling in HeLa cells. Wnt luciferase reporter assay in HeLa cells co-transfected with the indicated constructs. Wnt3a was added as conditioned medium. RLU, relative light units.

Figure 15: Futrin expression is deregulated in various human tumors

The expression of *Futrin 1, 2, 3 and-4* or ubiquitin (to show

equal loading) was analysed by radioactive hybridisation on arrayed mRNAs (Clontech, Cancer Profiling Array II) from normal and cancerous tissue samples from different patients. Abbreviations N, normal tissues; T, tumor tissues.

Figure 16: Expression of human *R-spondins in* tumor samples

Dot blot analysis of human *Rspo1, 2 and 3* in normal and tumour samples. The same CDNA samples (Cancer Profiling Array II, Clontech) were hybridized with human *Rspo1, 2, 3* and *ubiquitin* probes. (top) The Cancer Profiling Array contains pairs of cDNAs from tumor and corresponding normal tissue samples from individual patients and spotted side-by-side as indicated. Organ abbreviations are: Br, breast; ov, ovary; co, colon; st, stomach; lu, lungs; kidney; bi, bleeder, vu, vulva; pr, prostate; tr, trachea; liv, liver; ut, uterus; ce, cervix; re, rectum; th, thyroid gland; te, testis; sk, skin; sin, small intestine, pa, pancreas.

Figure 17: Interaction of R-spondins with components of the Wnt/ß-catenin signalling pathway

(A-C) Wnt luciferase reporter assay in 293T cells co-transfected with the indicated constructs. Results are indicated as fold-stimulation over reporter alone. DNA doses were 5 ng *Wnt1*, 1 ng *Fz8*, 3ng *LRP6*, 10 ng *axin*, 10 ng *dntcf3*, 5ng *dkk1*, 10 ng *Xdsh*, 1 ng *Wnt3a*.

The present invention relates to a diagnostic composition comprising:

> (a)   at least one nucleic acid molecule comprising the nucleotide sequence encoding Futrin 1, 2, 3 or 4 as depicted in Figure 3; and/or
>
> (b)   at least one polypeptide molecule comprising the amino acid sequence encoding Futrin 1,2,3 or 4 as depicted in Figure 4 or 6a; and/or
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> (c)   at least one nucleic acid molecule the complementary

strand of which hybridizes to a nucleic acid molecule of (a) and which encodes a polypeptide with the biological activity of Futrin 1, 2, 3 or 4; and/or

(d)   at least one fragment of (a), (b) or (c) having the biological activity of Futrin 1, 2, 3 or 4;

(e)   at least one nucleic acid molecule the sequence of which differs from the sequence of the nucleic acid molecule of (a), (c) or (d) due to the degeneracy of the genetic code, and/or

(f)   at least one ligand capable of specifically binding to the molecule of (a), (b), (c), (d) or (e).

As used herein the term „polypeptide„ not only refers to polypeptids encoded by the nucleotide/amino acid sequences as depicted in Figure 3 and/or 4 but also to polypeptides differing in amino acid sequence due to insertion, deletion and/or substitution of one ore more amino acids and showing at least one biological activity of a Futrin, e.g. the ability to promote Wnt signalling. Preferably, the related nucleic acids and/or polypeptides are nucleic acids and/or polypeptides the sequence of which shows an identity of at least 40%, in particular an identity of at least 65%, preferably of at least 80% and, particularly preferred, of at least 90% to the amino acid sequences of the polypeptides encoded by the nucleotide sequences shown in Figure 3.

The nucleic acid molecules useful as probes can be both DNA and RNA molecules, preferably they are single-stranded DNA molecules. They can be isolated from natural sources or can be synthesized according to know methods.

As a hybridization probe nucleic acid molecules can be used, for example, that have a nucleotide sequence which is exactly or basically complementary to a nucleotide sequence as depicted in Figures 3 and 4 or 6a, respectively, or parts of these sequences. The fragments used as hybridization probe can

be synthetic fragments that were produced by means of conventional synthetic methods.

As used herein, the term „hybridizing„ relates to hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook et al., Molecular Cloning, A Laboratory Manual 2nd edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. However, in certain cases, a hybridizing nucleic acid molecule can also be detected at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°Cin a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 9.2M NaH_2PO_4; 0.02M EDTA, pH7.4), 0.5% SDS, 30% formamide, 100 μg/ml salmon sperm blocking DNA, following by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

The term „ligand„ as used herein refers to any molecule which is capable of specifically binding to Futrin 1,2,3, or 4, thus allowing to determine the level of receptor molecules. Examples of such molecules include antibodies, oligonucleotides, proteins or small molecules. The molecule can be the natural ligand of Futrins, or can be closely

related to said ligand, e.g., a fragment of the ligand, or a natural substrate, a structural or functional mimetic; see, e.g., Coligan, Current Protocols in Immunology 1(2) (1991); Chapter 5. In either case, the molecule can be isolated or rationally designed using known techniques; see also infra.

Preferably, the ligand is an antibody. The term „antibody„, preferably, relates to antibodies which consist essentially of pooled monoclonal antibodies with different epitopic specifities, as well as distinct monoclonal antibody preparations. Monoclonal antibodies are made from an antigen containing Futrin 1,2,3, or 4 or fragments thereof by methods well known to those skilled in the art (see, e.g., Köhler et al., Nature 256 (1975), 495). As used herein, the term „antibody„ (Ab) or „monoclonal antibody„ (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab') 2 fragments) which are capable of specifically binding to Futrin 1, 2, 3 and/or 4. Fab and f(ab')2 fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24: 316-325 (1983)). Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimerical, single chain, and humanized antibodies.

For certain purposes, e.g. diagnostic methods, the nucleic acid molecule used as probe or the ligand, e.g., antibody, can be detectably labeled, for example, with a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate, or an enzyme.

The nucleic acid molecules can be used, for example, as probes or primers in the diagnostic assays described below and allow, e.g., the analysis of the expression of Futrin 1,2,3, or -4 by

determining the mRNA level or the determination of mutations within the coding region or regulatory regions leading to polypeptide molecules with altered, e.g. destroyed, activity, or leading to altered expression. Preferably, the nucleic acid molecules are oligonucleotides having a length of at least 10, in particular of at least 15 and particularly preferred of at least 50 nucleotides. These nucleic acid molecules of the invention can also be used, for example, as primers for a PCR reaction.

The present invention also relates to the use of a nucleic acid molecule or ligand as defined above for the preparation of a diagnostic composition for the diagnosis of a disease associated with (a) aberrant expression of Futrin 1,2,3, or -4 and/or (b) aberrant activity of a Futrin 1,2,3, or -4 polypeptide.

In a preferred embodiment, the target to which the nucleic acid molecule hybridizes is an mRNA.

The present invention also provides a method of diagnosing a disease associated with (a) aberrant expression of Futrin 1,2,3, or -4 and/or (b) aberrant activities or amounts of a Futrin 1,2,3, or -4 polypeptide in a subject comprising:
    (a) determining (a) the amount of expression of Futrin 1,2,3, or -4 and/or (b) the amount of biologically active Futrin 1, 2, 3 and/or 4 polypeptide in a biological sample; and
    (b) diagnosing a disease associated with (a) aberrant expression of *Futrin 1, 2, 3 and/or 4* and/or (b) aberrant activites or amounts of a Futrin 1, 2, 3 and/or 4 polypeptide or a risk for the development of such diasease based on an altered amount of expression of *Futrin 1, 2, 3 and/or 4* and/or (b) altered activities or amounts of biologically active Futrin 1, 2, 3 and/or 4 polypeptide compared to a control.

Suitable assay formats are well known to the person skilled in the art and, in addition, described below. Suitable positive control samples expressing human Futrin proteins are, e.g., HEK 293 cells.

The Futrin 1,2,3, or 4 polypeptide or the corresponding mRNA, e.g. in biological fluids or tissues, may be detected directly in situ, e.g. by in situ hybridization or it may be isolated from other cell components by common methods known to those skilled in the art before contacting with a probe. Detection methods include Northern Blot analysis, RNase protection, in situ methods, e.g. in situ hybridization, in vitro amplification methods (PCR, LCR, QRNA replicase or RNA-transcription/amplification (TAS, 3SR), reverse dot blot disclosed in EP-B1 O 237 362), immunoassays, Western Blot and other detection assays that are known to those skilled in the art.

The probe (e.g. a specific antibody or specific oligonucleotide) of the diagnostic composition can be detectably labeled. In a preferred embodiment, said diagnostic composition contains an anti- Futrin 1, 2, 3 and/or 4 antibody and allows said diagnosis, e.g., by ELISA and contains the antibody bound to a solid support, for example, a polystyrene microtiter dish or nitrocellulose paper, using techniques known in the art. Alternatively, said diagnostic compositions are based on a RIA and contain said antibody marked with a radioactive isotope. Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{125}I, ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{112}In), and technetium rhodamine, and biotin. In addition to assaying Futrin levels in a biological sample, the polypeptide can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels

include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma. A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I, ^{112}In, ^{99}mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99}mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific Futrin polypeptide. In vivo tumor imaging is, e.g., described in S.W. Burchiel et al., „Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments". (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B.A. Rhodes, eds., Masson Publishing Inc. (1982)).

In a further aspect, the present invention, relates to a method for identifying a binding partner to a Futrin 1, 2, 3 and/or -4 polypeptide comprising:
  (a) contacting said polypeptide with a compound to be screened; and
  (b) determining whether the compound effects an activity of the polypeptide.

The invention also includes a method of identifying compounds which bind to a Futrin 1, 2, 3 and/or 4 polypeptide comprising the steps of:

(a) incubating a candidate binding compound with said polypeptide; and

(b) determining if binding has occurred.

Futrin 1, 2, 3 or -4 polypeptides may be used to screen for proteins or other compounds that bind to Futrin 1, 2, 3 or -4 or for proteins or other compounds to which Futrin1, 2, 3 and/or 4 bind. The binding of Futrin1, 2, 3 or -4 and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of Futrin 1, 2, 3 or 4 or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., ligands), or small molecules.

Preferably, the molecule is closely related to the natural ligand of Futrin 1, 2, 3 or -4, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic; see, e.g., Coligan, Current Protocols in Immunology 1(2) (1991); Chapter 5.

Preferably, the screening for these molecules involves producing appropriate cells which express Futrin 1, 2, 3 and/or 4 either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing Futrin 1, 2, 3 and/or -4 (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of Futrin 1, 2, 3 and/or -4.

The assay may simply test binding of a candidate compound to Futrin 1, 2, 3 and/or 4, wherein binding is detected by a label, or in an assay involving competition with a labeled

competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to Futrin 1, 2, 3 and/or 4. Suitable assays to analyze the activity of Futrin 1, 2, 3 and/or 4 include Wnt-inducible luciferase reporter assays in transfected HEK 293 cells, where Futrin 1, 2, 3 and/or 4 synergizes with Wnt to enhance a Wnt-induced signal, such as is shown in Figure 4.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing Futrin 1, 2, 3 and/or 4, measuring Futrin/molecule activity or binding, and comparing the Futrin/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure Futrin 1, 2, 3 and/or 4 level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure Futrin 1, 2, 3 and/or 4 level or activity by either binding, directly or indirectly, to Futrin 1, 2, 3 and/or 4 or by competing with Futrin 1, 2, 3 and/or 4 for a substrate. All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., elimination of a tumor, support of regenerative processes etc.) by modulating, preferably activating the Futrin 1, 2, 3 and/or 4 molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of Futrin 1, 2, 3 and/or 4 from suitably manipulated cells or tissues.

Moreover, the invention includes a method of identifying activators/agonists or inhibitors/antagonists of a Futrin 1, 2, 3 and/or 4 polypeptide comprising the steps of:
   (a) incubating a candidate compound with said polypeptide;

(b) assaying a biological activity, and

(c) determining if a biological activity of said polypeptide
     has been altered.

Suitable assays to analyze the activity of Futrin 1, 2, 3
and/or 4 include Wnt-inducible luciferase reporter assays in
transfected HEK 293 cells, where Futrin 1, 2, 3 and/or 4
synergizes with Wnt to enhance a Wnt-induced signal, such as
is shown in Figure 4.

In a further embodiment, the present invention relates to
method of identifying and obtaining a drug candidate for
therapy of diseaseas associated with (a) aberrant expression of
Futrin 1, 2, 3 and/or 4 and/or (b) aberrant activities or
amounts of a Futrin 1, 2, 3 and/or 4 polypeptide comprising the
steps of

(a) contacting a Futrin 1, 2, 3 and/or 4 polypeptide or a
     cell expressing said polypeptide, and optionally the
     corresponding ligand(s), in the presence of components
     capable of providing a detectable signal in response to
     binding to said drug candidate to be screened; and

(b) detecting presence or absence of a signal or increase
     of the signal generated, wherein the presence or increase
     of the signal is indicative for a putative drug.

Suitable assays to analyze the activity of Futrin 1, 2, 3
and/or 4 include Wnt-inducible luciferase reporter assays in
transfected HEK 293 cells, where Futrin 1, 2, 3 and/or 4
synergizes with Wnt to enhance a Wnt-induced signal, such as
is shown in Figure 4.

The drug candidate may be a single compound or a plurality of
compounds. The term "plurality of compounds" in a method of
the invention is to be understood as a plurality of substances
which may or may not be identical.

Said compound or plurality of compounds may be chemically synthesized or microbiologically produced and/or comprised in, for example, samples, e.g., cell extracts from, e.g., plants, animals or microorganisms. Furthermore, said compound(s) may be known in the art but hitherto not known to be capable of suppressing or activating Futrin1, 2, 3 and/or 4 polypeptides. The reaction mixture may be a cell free extract or may comprise a cell or tissue culture. Suitable set ups for the method of the invention are known to the person skilled in the art and are, for example, generally described in Alberts et al., Molecular Biology of the Cell, third edition (1994) and in the appended examples. The plurality of compounds may be, e.g., added to the reaction mixture, culture medium, injected into a cell or otherwise applied to a transgenic animal. The cell or tissue that may be employed in the method of the invention preferably is a host cell, mammalian cell or non-human transgenic animal.

If a sample containing a compound or a plurality of compounds is identified in the method of the invention, then it is either possible to isolate the compound from the original sample identified as containing the compound capable of suppressing or activating a Futrin 1, 2, 3 and/or 4 polypeptide, or one can further subdivide the original sample, for example, if it consists of a plurality of different compounds, so as to reduce the number of different substances per sample and repeat the method with the subdivisions of the original sample. Depending on the complexity of the samples, the steps described above can be performed several times, preferably until the sample identified according to the method of the invention only comprises a limited number of or only one substance(s). Preferably said sample comprises substances of similar chemical and/or physical properties, and most preferably said substances are identical.

Several methods are known to the person skilled in the art for producing and screening large libraries to identify compounds having specific affinity for a target. These methods include the phage-display method in which randomized peptides are displayed from phage and screened by affinity chromatography to an immobilized receptor; see, e.g., WO 91/17271, WO 92/01047, US-A-5,223,409. In another approach, combinatorial libraries of polymers immobilized on a chip are synthesized using photolithography; see, e.g., US-A-5,143,854, WO 90/15070 and WO 92/10092. The immobilized polymers are contacted with a labeled receptor and scanned for label to identify polymers binding to the receptor. The synthesis and screening of peptide libraries on continuous cellulose membrane supports that can be used for identifying binding ligands of the Futrin1, 2, 3 and/or -4 polypeptides and, thus, possible inhibitors and activators is described, for example, in Kramer, Methods Mol. Biol. 87 (1998), 25-39. This method can also be used, for example, for determining the binding sites and the recognition motifs in the Futrin 1, 2, 3 and/or -4 polypeptide. In like manner, the substrate specificity of the DnaK chaperon was determined and the contact sites between human interleukin-6 and its receptor; see Rudiger, EMBO J. 16 (1997), 1501-1507 and Weiergraber, FEBS Lett. 379 (1996), 122-126, respectively. Furthermore, the above-mentioned methods can be used for the construction of binding supertopes derived from the Futrin 1, 2, 3 or 4 polypeptide. A similar approach was successfully described for peptide antigens of the anti-p24 (HIV-1) monoclonal antibody; see Kramer, Cell 91 (1997), 799-809. A general route to fingerprint analyses of peptide-antibody interactions using the clustered amino acid peptide library was described in Kramer, Mol. Immunol. 32 (1995), 459-465. In addition, antagonists of a Futrin 1, 2, 3 and/or 4 polypeptide can be derived and identified from monoclonal antibodies that specifically react with a Futrin 1, 2, 3 and/or 4 polypeptide in accordance with the methods as described in Doring, Mol. Immunol. 31 (1994), 1059-1067.

All these methods can be used in accordance with the present invention to identify activators/agonists and inhibitors/antagonists of a Futrin 1, 2, 3 and/or 4 polypeptide.

Various sources for the basic structure of such an activator or inhibitor can be employed and comprise, for example, mimetic analogs of a Futrin 1, 2, 3 and/or 4 polypeptide. Mimetic analogs of a Futrin 1, 2, 3 and/or 4 polypeptide or biologically active fragments thereof can be generated by, for example, substituting the amino acids that are expected to be essential for the biological activity with, e.g., stereoisomers, i.e. D-amino acids; see e.g., Tsukida, J. Med. Chem. 40 (1997), 3534-3541. Furthermore, in case fragments are used for the design of biologically active analogs pro-mimetic components can be incorporated into a peptide to reestablish at least some of the conformational properties that may have been lost upon removal of part of the original polypeptide; see, e.g., Nachman, Regul. Pept. 57 (1995), 359-370. Furthermore, a Futrin 1, 2, 3 and/or 4 polypeptide can be used to identify synthetic chemical peptide mimetics that bind to or can function as a ligand, substrate or binding partner of said polypeptide(s) as effectively as does the natural polypeptide; see, e.g., Engleman, J. Clin. Invest. 99 (1997), 2284-2292. For example, folding simulations and computer redesign of structural motifs of a Futrin 1, 2, 3 and/or 4 polypeptide can be performed using appropriate computer programs (Olszewski, Proteins 25 (1996), 286-299; Hoffman, Comput. Appl. Biosci. 11 (1995), 675-679). Computer modeling of protein folding can be used for the conformational and energetic analysis of detailed peptide and protein models (Monge, J. Mol. Biol. 247 (1995), 995-1012; Renouf, Adv. Exp. Med. Biol. 376 (1995), 37-45). In particular, the appropriate programs can be used for the identification of interactive sites of a Futrin 1, 2, 3 and/or 4 polypeptide and its ligand or other interacting proteins by computer assistant searches for complementary

peptide sequences (Fassina, Immunomethods 5 (1994), 114-120. Further appropriate computer systems for the design of protein and peptides are described in the prior art, for example in Berry, Biochem. Soc. Trans. 22 (1994), 1033-1036; Wodak, Ann. N. Y. Acad. Sci. 501 (1987), 1-13; Pabo, Biochemistry 25 (1986), 5987-5991. The results obtained from the above-described computer analysis can be used for, e.g., the preparation of peptide mimetics of a Futrin 1, 2, 3 and/or 4 polypeptide or fragments thereof. Such pseudopeptide analogues of the natural amino acid sequence of the protein may very efficiently mimic the parent protein (Benkirane, J. Biol. Chem. 271 (1996), 33218-33224). For example, incorporation of easily available achiral ω -amino acid residues into a Futrin 1, 2, 3 or -4 polypeptide or a fragment thereof results in the substitution of amide bonds by polymethylene units of an aliphatic chain, thereby providing a convenient strategy for constructing a peptide mimetic (Banerjee, Biopolymers 39 (1996), 769-777). Superactive peptidomimetic analogues of small peptide hormones in other systems are described in the prior art (Zhang, Biochem. Biophys. Res. Commun. 224 (1996), 327-331). Appropriate peptide mimetics of a Futrin 1, 2, 3 and/or 4 polypeptide can also be identified by the synthesis of peptide mimetic combinatorial libraries through successive amide alkylation and testing the resulting compounds, e.g., for their binding and immunological properties. Methods for the generation and use of peptidomimetic combinatorial libraries are described in the prior art, for example in Ostresh, Methods in Enzymology 267 (1996), 220-234 and Dorner, Bioorg. Med. Chem. 4 (1996), 709-715. Furthermore, a three-dimensional and/or crystallographic structure of a Futrin 1, 2, 3 and/or 4 polypeptide can be used for the design of peptide mimetic inhibitors of the biological activity of the polypeptide (Rose, Biochemistry 35 (1996), 12933-12944; Rutenber, Bioorg. Med. Chem. 4 (1996), 1545-1558).

It is also well known to the person skilled in the art, that it is possible to design, synthesize and evaluate mimetics of

small organic compounds that, for example, can act as a substrate or ligand to a Futrin 1, 2, 3 and/or 4 polypeptide. For example, it has been described that D-glucose mimetics of hapalosin exhibited similar efficiency as hapalosin in antagonizing multidrug resistance assistance-associated protein in cytotoxicity; see Dinh, J. Med. Chem. 41 (1998), 981-987.

The nucleic acid molecule encoding a Futrin 1, 2, 3 and/or 4 polypeptide can also serve as a target for activators and inhibitors. Activators may comprise, for example, proteins that bind to the mRNA of a gene encoding a Futrin 1, 2, 3 and/or 4 polypeptide, thereby stabilizing the native conformation of the mRNA and facilitating transcription and/or translation, e.g., in like manner as Tat protein acts on HIV-RNA. Furthermore, methods are described in the literature for identifying nucleic acid molecules such as an RNA fragment that mimics the structure of a defined or undefined target RNA molecule to which a compound binds inside of a cell resulting in retardation of cell growth or cell death; see, e.g., WO 98/18947 and references cited therein. These nucleic acid molecules can be used for identifying unknown compounds of pharmaceutical interest, and for identifying unknown RNA targets for use in treating a disease. These methods and compositions can be used in screening for novel or for identifying compounds useful to alter expression levels of polypeptids encoded by a nucleic acid molecule. Alternatively, for example, the conformational structure of the RNA fragment which mimics the binding site can be employed in rational drug design to modify known drugs to make them bind more avidly to the target. One such methodology is nuclear magnetic resonance (NMR), which is useful to identify drug and RNA conformational structures. Still other methods are, for example, the drug design methods as described in WO 95/35367, US-A-5,322,933, where the crystal structure of the RNA fragment can be deduced

and computer programs are utilized to design novel binding
compounds.

The compounds which can be tested and identified according to
a method of the invention may be expression libraries, e.g.,
cDNA expression libraries, peptides, proteins, nucleic acids,
antibodies, small organic compounds, hormones,
peptidomimetics, PNAs or the like (Milner, Nature Medicine 1
(1995), 879-880; Hupp, Cell 83 (1995), 237-245; Gibbs, Cell 79
(1994), 193-198 and references cited supra). Furthermore,
genes encoding a putative regulator of a Futrin 1, 2, 3 and/or
4 polypeptide and/or which excert their effects up- or
downstream a Futrin 1, 2, 3 and/or 4 polypeptide may be
identified using, for example, insertion mutagenesis using,
for example, gene targeting vectors known in the art. Said
compounds can also be functional derivatives or analogues of
known inhibitors or activators. Such useful compounds can be
for example transacting factors which bind to a Futrin 1, 2, 3
and/or 4 polypeptide or regulatory sequences of the gene
encoding it. Identification of transacting factors can be
carried out using standard methods in the art (see, e.g.,
Sambrook, supra). To determine whether a protein binds to the
protein itself or regulatory sequences, standard native gel-
shift analyses can be carried out. In order to identify a
transacting factor which binds to the protein or regulatory
sequence, the protein or regulatory sequence can be used as an
affinity reagent in standard protein purification methods, or
as a probe for screening an expression library. The
identification of nucleic acid molecules which encode
polypeptides which interact with a Futrin 1, 2, 3 and/or 4
polypeptide described above can also be achieved, for example,
as described in Scofield (Science 274 (1996), 2063-2065) by use
of the so-called yeast "two-hybrid system". In this system the
Futrin1, 2, 3 or 4 polypeptide or a smaller part thereof is
linked to the DNA-binding domain of the GAL4 transcription
factor. A yeast strain expressing this fusion polypeptide and

comprising a lacZ reporter gene driven by an appropriate promoter, which is recognized by the GAL4 transcription factor, is transformed with a library of cDNAs which will express plant proteins or peptides thereof fused to an activation domain. Thus, if a peptide encoded by one of the cDNAs is able to interact with the fusion peptide comprising a peptide of a Futrin 1, 2, 3 and/or 4 polypeptide, the complex is able to direct expression of the reporter gene. In this way the nucleic acid molecules encoding Futrin1, 2, 3 and 4, respectively, and the encoded peptide can be used to identify peptides and proteins interacting with a Futrin1, 2, 3 and/or 4 polypeptide.

Once the transacting factor is identified, modulation of its binding to or regulation of expression of a Futrin 1, 2, 3 and/or 4 polypeptide can be pursued, beginning with, for example, screening for inhibitors against the binding of the transacting factor to a Futrin1, 2, 3 or 4 polypeptide. Activation or repression of a Futrin 1, 2, 3 and/or 4 polypeptide could then be achieved in animals by applying the transacting factor (or its inhibitor) or the gene encoding it, e.g. in an expression vector. In addition, if the active form of the transacting factor is a dimer, dominant-negative mutants of the transacting factor could be made in order to inhibit its activity. Furthermore, upon identification of the transacting factor, further components in the signal cascade leading to activation (e.g. signal transduction) or repression of a gene involved in the control of a Futrin 1, 2, 3 and/or 4 polypeptide then can be identified. Modulation of the activities of these components can then be pursued, in order to develop additional drugs and methods for modulating the metabolism of protein degradation in animals. Thus, the present invention also relates to the use of the two-hybrid system as defined above for the identification of activators or inhibitors of a Futrin 1, 2, 3 and/or 4 polypeptide.

The compounds isolated by the above methods also serve as lead compounds for the development of analog compounds. The analogs should have a stabilized electronic configuration and molecular conformation that allows key functional groups to be presented to a Futrin 1, 2, 3 and/or 4 polypeptide or its ligand in substantially the same way as the lead compound. In particular, the analog compounds have spatial electronic properties which are comparable to the binding region, but can be smaller molecules than the lead compound, frequently having a molecular weight below about 2 kD and preferably below about 1 kD. Identification of analog compounds can be performed through use of techniques such as self-consistent field (SCF) analysis, configuration interaction (CI) analysis, and normal mode dynamics analysis. Computer programs for implementing these techniques are available; e.g., Rein, Computer-Assisted Modeling of Receptor-Ligand Interactions (Alan Liss, New York, 1989). Methods for the preparation of chemical derivatives and analogues are well known to those skilled in the art and are described in, for example, Beilstein, Handbook of Organic Chemistry, Springer edition New York Inc., 175 Fifth Avenue, New York, N.Y. 10010 U.S.A. and Organic Synthesis, Wiley, New York, USA. Furthermore, said derivatives and analogues can be tested for their effects according to methods known in the art; see also supra. Furthermore, peptidomimetics and/or computer aided design of appropriate derivatives and analogues can be used, for example, according to the methods described above.

Once the described compound has been identified and obtained, it is preferably provided in a therapeutically acceptable form.

Accordingly, the present invention also relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a Futrin 1, 2, 3 and/or 4 polypeptide, a Futrin 1, 2, 3 and/or 4 polypeptide itself, recombinant vector (for

examples, see below), antibody, activator/agonist, inhibitor/antagonist and/or binding partner of a Futrin 1, 2, 3 and/or 4 polypeptide and a pharmaceutically acceptable excipient, diluent or carrier.

Preferably, for therapeutic purposes, the Futrin 1, 2, 3 and/or 4 polypeptide is recombinantly produced by use of the nucleic acid sequences shown in Figures 1 and 2. Suitable vectors for recombinant expression are known to the person skilled in the art. Preferably, they are plasmids, cosmids, viruses, bacteriophages and other vectors usually used in the field of genetic engineering. Vectors suitable for use in the present invention include, but are not limited to the T7-based expression vector for expression in mammalian cells and baculovirus-derived vectors for expression in insect cells. Preferably, the nucleic acid molecule of the invention is operatively linked to the regulatory elements in the recombinant vector of the invention that guarantee the transcription and synthesis of an mRNA in prokryotic and/or eukaryotic cells that can be translated. The nucleotide sequence to be transcribed can be operably linked to a promoter like a T7, metallothionein I or polyhedrin promoter. The host cells used for recombinant expression are prokaryotic or eukaryotic cells, for example mammalian cells, bacterial cells, insect cells or yeast cells. The polypeptide is isolated from the cultivated cells and/or the culture medium. Isolation and purification of the recombinantly produced polypeptide may be carried out by conventional means including preparative chromatography and affinity and immunological separations using, e.g., an anti-Futrin 1, 2, 3 or -4 antibody, or, e.g., can be substantially purified by the one-step method described in Smith and Johnson, Gene 67; 31-40 (1988).

Examples of suitable pharmaceutical carriers etc. are well known in the art and include phosphate buffered saline

solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions etc. Such carriers can be formulated by conventional methods and can be administered to the subject at a suitable dose. Administration of the suitable compositions may be effected by different ways, e.g. by intravenous, intraperetoneal, subcutaneous, intramuscular, topical or intradermal administration. The route of administration, of course, depends on the nature of the disease and the kind of compound contained in the pharmaceutical composition. The dosage regimen will be determined by the attending physician and other clinical factors. As is well known in the medical arts, dosages for any one patient depends on many factors, including the patient's size, body surface area, age, sex, the particular compound to be administered, time and route of administration, the kind and stage of the disease, e.g., tumor, general health and other drugs being administered concurrently.

The delivery of the nucleic acid molecules encoding a Futrin 1, 2, 3 and/or 4 polypeptide can be achieved by direct application or, preferably, by using a recombinant expression vector such as a chimeric virus containing these compounds or a colloidal dispersion system. Direct application to the target site can be performed, e.g., by ballistic delivery, as a colloidal dispersion system or by catheter to a site in artery. The colloidal dispersion systems which can be used for delivery of the above nucleic acid molecules include macromolecule complexes, nanocapsules, microspheres, beads and lipid-based systems including oil-in-water emulsions (mixed), micelles, liposomes and lipoplexes, The preferred colloidal system is a liposome. Organ-specific or cell-specific liposomes can be used in order to achieve delivery only to the desired tissue. The targeting of liposomes can be carried out by the person skilled in the art by applying commonly known methods. This targeting includes passive targeting (utilizing the natural tendency of the liposomes to distribute to cells

of the RES in organs which contain sinusoidal capillaries) or
active targeting (for example by coupling the liposome to a
specific ligand, e.g., an antibody, a receptor, sugar,
glycolipid, protein etc., by well known methods). In the
present invention monoclonal antibodies are preferably used to
target liposomes to specific tissues, e.g. tumor tissue, via
specific cell-surface ligands.

Preferred recombinant vectors useful for gene therapy are
viral vectors, e.g. adenovirus, herpes virus, vaccinia, or,
more preferably, an RNA virus such as a retrovirus. Even more
preferably, the retroviral vector is a derivative of a murine
or avian retrovirus. Examples of such retroviral vectors which
can be used in the present invention are: Moloney murine
leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV),
murine mammary tumor virus (MuMTV) and Rous sarcoma virus
(RSV). Most preferably, a non-human primate retroviral vector
is employed, such as the gibbon ape leukemia virus (GaLV),
providing a broader host range compared to murine vectors.
Since recombinant retroviruses are defective, assistance is
required in order to produce infectious particles. Such
assistance can be provided, e.g., by using helper cell lines
that contain plasmids encoding all of the structural genes of
the retrovirus under the control of regulatory sequences
within the LTR. Suitable helper cell lines are well known to
those skilled in the art. Said vectors can additionally
contain a gene encoding a selectable marker so that the
transduced cells can be identified. Moreover, the retroviral
vectors can be modified in such a way that they become target
specific. This can be achieved, e.g., by inserting a
polynucleotide encoding a sugar, a glycolipid, or a protein,
preferably an antibody. Those skilled in the art know
additional methods for generating target specific vectors.
Further suitable vectors and methods for in vitro- or in vivo-
gene therapy are described in the literature and are known to

the persons skilled in the art; see, e.g., WO 94/29469 or WO 97/00957.

In order to achieve expression only in the target organ, e.g., a tumor to be treated, the nucleic acid molecules encoding a Futrin 1, 2, 3 and/or 4 polypeptide can be linked to a tissue specific promoter and used for gene therapy. Such promoters are well known to those skilled in the art (see e.g. Zimmermann et al., (1994) Neuron 12, 11-24; Vidal et al.; (1990) EMBO J. 9, 833-840; Mayford et al., (1995), Cell 81, 891-904; Pinkert et al., (1987) Genes & Dev. 1, 268-76).

The present invention also relates to the use of the above compounds of the invention for the preparation of a pharmaceutical composition for treatment of a disease associated with (a) aberrant expression of Futrin 1, 2, 3 and/or 4 and/or genes involved into the Wnt signal cascade, and/or (b) aberrant activities or amounts of a Futrin 1, 2, 3 and/or 4 and/or a polypeptide involved into the Wnt signal cascade. In a preferred embodiment, said disease is a kidney, bone or muscle disease or tumor, preferably breast cancer, a colon carcinoma or a melanoma.

Finally, the present invention relates to the use of a nucleotide molecule encoding a polypeptide having a biological activity of Futrin 1, 2, 3 and/or 4, a Futrin 1, 2, 3 and/or 4 polypeptide, an activator/agonist of a Futrin 1, 2, 3 and/or 4 polypeptide or binding partner of said polypeptide(s) for the preparation of a pharmaceutical composition for inhibiting the Wnt signal cascade which might be useful for supporting regenerative processes in a patient, e.g. growth of tissue like muscle, bone, hair, etc.

The following examples illustrate the invention.

Example 1
Materials and Methods

(A) Isolation of Futrins (= *R-spondins*) and constructs

A Xenopus adult eye cDNA library in pCS2+ was used to prepare pools of about 250 colonies. Plasmid DNA from each pool was transiently transfected into 293T cells together with the Wnt receptor *frizzled8,* the Wnt reporter TOPFLASH (Korinek et al., Science 275 (1997), 1784-7) and pRL-TK (Promega) using FuGENE6 (Roche) transfection reagent. Luciferase assay was carried out 24 hours after transfection. A positive clone was isolated from the pool by sib selection. Human Rspo2 and 3 cDNAs were obtained from RZPD. Fragments of *hRspo1* and 4 were RT-PCR amplified from mRNA of 293T cells and used as hybridization probes. Full length mouse *Rspo1* and 2 were isolated from a mouse embryonic day 13.5 cDNA library. The sequence of X. *tropicalis Rspo3* was obtained from Sanger Institute database and a cDNA fragment was cloned by RT-PCR from X. *tropicalis* embryos. C-terminally Myc or FLAGtagged constructs and all deletion constructs were created by PCR. *Xenopus* Rspo2ΔC was cloned by deleting the last 37 amino acids. The Rspo3 cDNAs were cloned in pCS2+ and Bluescript vectors for use in gene expression and as probes, respectively.

(B) Cell culture, recombinant proteins and luciferase reporter assays

HEK293T, SHEP and HeLa cell lines were maintained in DMEM, 10% FCS and 10% CO_2. *Xenopus* Rspo2ΔC conditioned medium was produced by transient transfection in 293T cells. Mouse Wnt3a conditioned medium was produced from mouse L cells stably transfected with Wnt3a (ATCC#CRL-2647) (Shibamoto et al., Genes Cells 3 (1998), 659-670). Luciferase reporter assays in

293T cells were carried out in 96-well plates as described (Wu et al., Curr. Biol. 10 (2000), 1611-1614). Luciferase reporter assays in HeLa cells were carried out in 24 well plates in triplicates using Lipofectamine Plus transfection reagent (Invitrogen). Per well a total of 400 ng DNA were transfected, including 80ng *7lef-fos-Luc* (Novak et al., PNAS 95 (1998), 4374-4379), 10 ng *pRL-TK,* 10 ng mouse *frizzled8,* 2 ng mouse *lef1* and 300 ng pSuper plasmid DNAs. 3 days after transfection, either mouse *Wnt3a* conditioned medium or medium containing 30 mM LICl was added to stimulate Wnt signalling. 24 hours later, luciferase activity was determined using the Dual luciferase system (Promega).

(C) Embryos, explants, in situ hybridization and RNA synthesis

In vitro fertilisation, embryo culture, staging, microinjection and culture of *Xenopus* embryo explants were carried out as described (Gawantka et al., EMBO J. 14 (1995), 6268-79). Double- and single-labeling whole-mount in situ hybridization was carried out according to (Bradley et al., Development <u>122</u> (1996), 2739-50). A PCR fragment of *tropicalis Rspo3* cDNA was used for in situ hybridization on *Xenopus laevis* embryos. For vibratome sectioning, embryos were placed in embedding medium (0.4% gelatine, 30% albumin, 20% sucrose in PBS) and mounted in the presence of 2% glutaraldehyde. Sectioning was carried out using a VT100E vibratome (Leica). Brains of 4day *Xenopus* embryos were excised in 1x Barth solution and fixed for in situ hybridisation. Whole-mount in situ hybridisation of mouse embryos was performed according to previously described procedures (Koop et al., Mech. Dev. 59 (1996), 73-78). Preparation of mRNA for *Xenopus* injections was carried out using the MegaScript *in vitro* transcription kit (Ambion), according to the manufacturer's instructions.

(D) Morpholino antisense oligonucleotides and siRNA constructs

The 5' nucleotide sequence of an additional (pseudo-) allele for *Xenopus Rspo2* gene was obtained using 5' RACE (GeneRacer kit, Invitrogen). Based on these sequences, an antisense morpholino oligonucleotide targeting both pseudoalleles around the ATG start codon was designed (Rspo2Mo): GCCGTCCAAATGCAGTTTCAAC. pSuper constructs producing siRNA against human *Rspo 2,3* or a non-sense control were made according to Brummelkamp et al., Science 296 (2002), 550-3. The sequences are: human *Rspo2*, TCCCATTTGCAAGGGTTGT; human *Rspo3*, AGCTGACTGTGATACCTGT; non-sense control, ACTACCGTTGTTATAGGTG.

(E) Immunohistochemistry, Western blot and dot blot analysis

Immunohistochemistry to detect ß-catenin in SHEP cells was carried out according to (Scheiffele et al., J. Cell. Biol. <u>140</u> (1998), 795-806) using anti-ß-catenin antibody (Transduction laboratories, Newington). For detection of tagged Rspo proteins or loading controls on Western blot, anti-Myc (clone 9E10), anti-FLAG (M2, SIGMA) monoclonal antibodies, chick anti-GFP (Chemicon, Hampshire) and mouse anti-a-tubulin (SIGMA) antibodies were used. Chemiluminescence detection (SuperSignal® solution, Pierce) was carried out according to the manufacturer's instructions after incubation of blots with anti-mouse IgG-HRP (Pierce). For *Rspo* expression analysis in tumour samples the Cancer Profiling Array II (Clontech, Palo Alto) was used and hybridization was carried out according the manufacturer's instructions.

(F) RT-PCR

RT-PCR assays were carried out as described (Dosch et al., Development 124 (1997), 2325-34; Glinka et al., Nature 389 (1997), 517-519); additional primers were: *Xenopus Rspo2*

(forward,   GAATGCCCAGAAGGATTTGC;   reverse,
GGGATGGTGTCTTTTGCTGG);   *Xenopus   Rspo3*   (forward,
GAAGCAAATTGGAGTCTGTCG;   reverse,   GATTGTTCTCAAACCCTTCAGG);
human *Rspo1* (forward, ACAGACACAAGACACACACGC; reverse,
TGTCTTCTGGTGGCCTCAG);   human   *Rspo2*   (forward,
CCGAGCCCCAGATATGAAC; reverse, TGACCAACTTCACATCCTTCC); human
Rspo3   (forward,   AGGGACTGAAACACGGGTC;   reverse,
TGTCTTCTGGTGGCCTCAG);   human   *Rspo4*   (forward,
AAGCTGGGACACAGCACAG; reverse, GAAGCCTTGGAGCCTTGTC).

Example 2
Isolation of a cDNA encoding Xenopus Futrin 1

A Xenopus adult eye cDNA library in the expression vector
pCS2+ was used to prepare pools of about 250 colonies, and
plasmid DNA from each pool was transiently transfected into
293T cells together with the Wnt receptor frizzled8, the Wnt
reporter TOP-FLASH (Korinek et al. Science 275 (1997) 1784-
1787) and Renilla-luciferase for normalization, in 96-well
plates using FuGENE 6 (Roche, Basel). After 24 hours relative
luciferase activity was determined. One pool yielding a signal
above background was identified (Figures 1 and 2A) and a gene
harboring this activity was isolated from the pool by sib
selection. Sequencing analysis showed it represents Xenopus
futrin 1. Database searches revealed four closely related
genes in human, called hfutrin 1, 2, 3 and 4 (Figures 3 and 4
or 6a).

Xenopus futrin 1 (Rspo2) is predicted to encode a secreted
protein with 243 amino acids (mature protein) and an
isoelectric point of 9.8. All R-spondins contain an N-
terminal signal peptide (SP), two furin-like domains (FU),
one thrombospondin type1 domain (TSP1) and a C-terminal low
complexity region enriched with positively charged amino

acids (C) (Figure 2F). The furin-like cysteine rich domain
is found in e.g. furin-like endoproteases, EGF receptor and
insulin receptor. In signal transduction by certain
receptor tyrosine kinases furin repeats are required for
receptor aggregation. TSP1 repeats are found in
Thrombospondin and other extracellular matrix proteins like
Mindin, F-spondin, SCO-spondin as well as in a number of
proteins involved in the complement cascade. Proteins
containing TSP1 repeats are involved in cell-cell
interaction, inhibition of angiogenesis and apoptosis
(Adams and Tucker, Dev. Dyn. 218 (2000), 280-99).

While *Xenopus* Rspo2 contains a predicted N-terminal signal
peptide, secreted protein is almost undetectable in the
medium of transiently transfected 293T cells. Since the C-
terminus is enriched with basic amino acids, which promotes
cell surface retention a C-terminally truncated protein was
tested. Rspo2ΔC is effectively secreted into the medium
from 293T cells (Figure 2B) and is functionally active
(Figure 2F). Since all R-spondins share the basic C-
terminus and since there are no obvious ER- or Golgi
retention signals, this suggests that the proteins are
normally associated with the cell surface.

Example 3

Futrins promote Wnt signalling

Xenopus Futrin1 and human Futrin1, 2, and 3 are able to
stimulate Wnt-responsive reporter expression in HEK 293T cells
when provided by transient transfection (Figures 2C and 5A).
In addition, they are able to enhance reporter expression
induced by Wnt (mouse Wnt1/3A) synergistically (Figures 2D and
5B). Cotransfection experiments in HEK239T cells were carried
out with the indicated genes and the Wnt reporter TOP-FLASH

(Korinek et al. Science <u>275</u> (1997) 1784-1787) and Renilla-luciferase for normalization, in 96-well plates using FuGENE 6 (Roche). After 24 hours relative luciferase activity was determined.

All tested members of the *Rspo* family (e.g. murine *Rspo1-3*, human *Rspo2, 3*) show equivalent effects (Figure 6A and data not shown). Rspo2 signalling is sensitive to the Wnt/ß-catenin pathway inhibitors dominant negative TCF and *dickkopf1* (Figure 6B). A synergistic signalling effect is observed when *Rspo2 is co*transfected with extracellular but not with intracellular components of the Wnt/ß-catenin pathway (Figure 6C). The greatest cooperation is reproducibly seen between Rspo2 and Wnts, either using conditioned media (Figure 2D) or following co-transfection (Figure 6C).

A hallmark of Wnt/ß-catenin signalling activation is the cytosolic accumulation of ß-catenin due to its stabilisation. Treatment of 293T cells with Wnt3a conditioned medium induces cytosolic ß-catenin after 1 hour and while recombinant Rspo2ΔC alone is not able to stabilize ß-catenin during this interval, it strongly enhances activity of Wnt3a to do so (Figure 2E, top). After 4 hours treatment, both Wnt3a and Rspo2ΔC conditioned media are able to induce ß-catenin accumulation to similar levels (Figure 2E, top). ß-catenin is known to enter the nuclei in response to Wnt stimulation and activate gene expression together with Lef/Tcf transcription factors. Treatment of SHEP cells by either Wnt3a or Rspo2ΔC conditioned media weakly induces ß-catenin nuclear localization, while co-treatment with Wnt3a and Rspo2ΔC strongly enhances nucleae accumulation (Figure 2E, bottom). It can be concluded that R-spondins represent a novel family of secreted proteins capable promoting Wnt/ß-catenin signalling.

To functionally study its signalling domains, serial

deletions of *Xenopus Rspo2* (Figure 2F) were created. As discussed, the basic C-terminus can be removed without loss of activity and this is also true for the TSP1 domain (Figure 2F). However, the furin-like·domains are necessary for Wnt/ß-catenin signalling since deletion of either the furin-1 or -2 domains abolishes the activity in reporter assays (Figure 2F).

Example 4
Futrins are required for full Wnt signalling

To test the requirement of Futrins in Wnt signalling, siRNA mediated gene knock-out was utilized (Brummelkamp et al., Science. 2002, 296(5567):550-3). Hela cells were transfected using Lipofectamine Plus with 80ng Wnt reporter 7LEF-Rev-fosLuc, 10 ng pRL-TK (Promega) and 300 ng pSuper constructs (Brummelkamp et al.) that produce either siRNA against human Futrin1 and 2, or a nonsense control. 7LEF-Rev-fosLuc reporter construct containing seven LEF binding sites in front of minimal fos promoter followed by firefly luciferase ORF was kindly provided by R. Grosschedl (Howard Hughes Medical Institute). pSuper constructs contain 19-nucleotide sequences from human Futrin1 (sequence: TCCCATTTGCAAGGGTTGT), human Futrin2 (sequence: AGCTGACTGTGATACCTGT) or control nonsense sequence (ACTACCGTTGTTATAGGTG).

One day after transfection medium was changed from 10% to 0.5% FCS. Three days after transfection, mouse Wnt3A conditioned medium or control medium from 293 cells was added to the culture to stimulate Wnt signalling. 24 hours later, luciferase activity was determined. As shown in Figure 7, Hela cells show reduced levels of Futrin 1 and 2, and Wnt signalling dropped by 50%, indicating that Futrins are required for full Wnt signalling. This effect can be

efficiently rescued by 5 ng recombinant mouse Futrin 1, attesting its specificity. Data are normalized to Renilla luciferase activity.

Example 5

Expression of *R-spondin* genes in *Xenopus* and mouse embryos

In *Xenopus* embryos, no maternal *Rspo2* RNA is detected by RT-PCR. Its zygotic expression starts at early gastrula stage and remains constant throughout neurulation and organogenesis (Figure 8A). By whole-mount in situ hybridization, weak expression of *Rspo2* is observed throughout the ectoderm of early gastrulae (not shown). During gastrulation strong expression is detected in the marginal zone in both deep and superficial layers, but is excluded from the Spemann organizer (Figure 8B). At late gastrula stage *Rspo2* expression persists in lateral plate mesoderm and becomes detectable in the anterior neural plate (Figure 8C). At stage 15 expression is seen in two longitudinal stripes along the neural plate (future roof plate), in the anterior neural plate and in lateral and posterior mesoderm (Figure 8D). Expression of *Rspo2* at tailbud stage (Figure 8F) is restricted to several regions of the brain, including diencephalon and midbrain-hindbrain boundary, pronephros and dorsal neural tube. Expression is also detected in the dorsal and ventral-most portions of somites, the dorsal fin and the proctodeum. Rspo2 expression in the brain of late tadpoles is mainly restricted to diencephalon, including the zona limitans intrathalamica (zli) (Figure 8H).

Xenopus Rspo3 expression is related to that of *Rspo2*. It is first detected at gastrula stage (not shown) and in neurulae it is expressed in the anterior border of the neural plate and posterior mesoderm (Figure 8E). At tailbud stage, it is

coexpressed with *Rspo2* in the central nervous system but shows additional expression in branchial arches and the tailbud (Figure 8G).

In mouse, Rspo3 transcripts are detected by in situ hybridization at day 7.5 in the primitive streak (Figure 8J) while expression of *Rspo1* and 2 is not detectable. At day 9.5, *Rspo1-3* show differential expression in various neural and mesodermal derivatives (Figure 8K-M), mainly along dorsal neural tube *(Rspo1* and 3), diencephalon *(Rspo1, 2, 3),* somites *(Rspo3)* and tailbud mesoderrn *(Rspo3).* In limb buds all three genes show prominent differential expression (Figure 8I), particularly, in the morphogenetically active region such as the apical ectodermal ridge (AER) *(Rspo2).*

Example 6
R-spondins are co-expressed with and regulated by *Wnts*

R-spondins not only show functional interaction with Wnt signalling, but also co-expression with *Wnt* genes in many regions during *Xenopus* and mouse embryonic development. In gastrula mesoderm of both *Xenopus* and mouse, *Rspo2* and *-3* are co-expressed with *XWnt8* and *mWnt3,* respectively. Similarly, at later stages, *R-spondin* family members are widely co-expressed with a number of *Wnt* genes e.g. in midbrain-hindbrain boundary, dorsal neural tube and limb bud and tail bud. A direct comparison between the expression patterns of *Xenopus Rspo2* and *Wnt8* and *Wnt3a* shows a large overlap (Figure 9A).

Indeed, Wnts are able to induce *Rspo* expression since *Xenopus* embryos injected with pCS-*Wnt8* or pCS-*ß-catenin* DNA upregulate both *Rspo2* and *Rspo3* by RT-PCR (Figure 9B).

Likewise, embryos injected with pCS-*Wnt8* or pCS-*Wnt3a* DNA show ectopic *Rspo2* expression by in situ hybridization (Figure 8C-E). The results indicate that the observed co-expression is due to regulation of *R-spondins* by *Wnts*. This is consistent with the observation that *Rspo1* expression is reduced in dorsal spinal cord of *Wnt1* or *Wnt3a* knockout mouse embryos.

Example 7

Futrin 1 (R-spondin 2) activates neural markers and regulates (promotes) muscle formation

Loss-of-function analysis in Xenopus embryos show that Futrin 1 is required for muscle formation. Injections of antisence morpholino oligo against futrin 1 (Fut1-Mo) cause downregulation of early muscle markers MyoD anf Myf5 and induce muscle defects (Figure 10A). The specificity of this effect was documented, first, by the ability of Fut1-Mo to inhibit translation of the cognate DNA construct when overexpressed in embryos (Figure 10B) and, second, by the ability of XFut1 mRNA to rescue the effect of Fut1-Mo (Figure 10C).

When the Wnt/ß-catenin pathway is overactivated in *Xenopus* embryos a variety of responses are observed: i) mRNA injection of pathway activators typically induces secondary embryonic axes in whole embryos and anterior neural markers in animal caps and whole embryos; ii) DNA injection of pathway activators driving expression after MBT, posteriorizes the central nervous system (CNS). To test if *Rspo2* is able to mimic any of these effects synthetic mRNA was microinjected in *Xenopus* embryos. However, *Rspo2* mRNA injection does not induce secondary axes in whole embryos and

injection of *pCS-Rspo2* DNA does not posteriorize CNS, since heads are normal sized, *Otx2* expression is expanded and *en2* unaffected (Figure 11D, H).

In animal caps *Rspo2* induces the pan-neural markers *NCAM* and *N-tubulin* and the anterior neural marker, *Otx2*, as do *Xwnt8* and *ß-catenin* (Figure 11A). Similarly, in whole embryos injected with *Rspo2* mRNA, ectopic cement glands and lateral expansion of the neural plate are observed at the injected side, as shown by expression of neural markers *Sox3, Otx2, not2, en2* and *Rx1* (Figures 11B-H). Ectopic Otx2 expression is observed already in gastrula stage embryos (Figure 11I+J). These results are consistent with the ability of Wnt/ß-catenin signalling to block BMP4 expression and thereby to activate neural development.

To further analyze the mRNA overexpression effect of Rspo2 an BMP4, Activin, Nodal and FGF signaling, animal cap assays were carried out and tested for the induction of target genes by three growth factor signals (Figure 12). Rspo2 expectedly blocks BMP4 mediated *Xvent2* expression but surprisingly also inhibits Activin and Nodal mediated *Xbra* induction (Figure 12A-C). This is unlike *XWnt8* and *ß-catenin* mRNA injections, which do not affect *Xbra* induction by Activin (Figure 12B). In contrast to signaling by three TGF-ß type growth factors, FGF8 induced *Xbra* expression is unaffected by overexpressed *Rspo2* (Figure 12D). It can be concluded that *Rspo2* overexpression in addition to activating the Wnt/ß-catenin pathway, is also able to interfere with signaling by three TGF-ß family growth factors.

Another well known effect of zygotic Wnt/ß-catenin signalling is its ability to promote myogenesis. For example, *XWnt8* can induce muscle formation in ventral mesodermal cells. When ventral marginal zones (VMZs) from

Rspo2 injected embryos are dissected and cultured until stage 40, they elongate, form tail like structures, and are contractile. This phenotype is indistinguishable from control lateral marginal zone explants (LMZs), which typically differentiate muscle (Fig. 4K-L). In situ hybridization confirmed induction of *muscle actin* in both *Wnt8* and *Rspo2* injected VMZs but not in control (preprolactin-injected) VMZs (Figure 11M). Since *R-spondins* are able to enhance Wnt signalling in 293T cells, their cooperation in *Xenopus* myogenesis was tested. Myf5 is a myogenic marker characteristically expressed in lateral mesoderm. However, it is excluded from dorsal mesoderm, and dorsal marginal zone (DMZ) explants express only little myf5 as determined by RT-PCR (Figure 11N). In DMZs from embryos injected with DNA constructs driving post MBT expression, myf5 is weakly induced by *Rspo2*, moderately by *Wnt8* and strongly by their combination (Figure 11N, top). The myogenesis promoting effect of *Rspo2* is repressed by dominant negative *dishevelled (Xddl), dkkl* and GSK-3ß, which all block Wnt signalling (Figure 11N, bottom). In summary, the results suggest that *Rspo2* can promote myogenesis via the Wnt/ß-catenin pathway.

Example 8
R-spondin2 is required for Wnt/ß-catenin-mediated myogenesis

To investigate the physiological role of Rspo2 during *Xenopus* embryogenesis, antisense morpholino oligonucleotides were injected (Rspo2Mo). The ability of Rspo2Mo to block Rspo2 protein production is demonstrated by Western blot (Figure 13A). Injection of this Morpholino into one dorso-animal blastomere at eight cell stage results in eye defects, although the expression of early

eye- *(Rx1, Pax6)*, anterior neural (Otx2) and pan-neural markers *(Sox3)* *is* not obviously affected (not shown).

Equatorial Injection of Rspo2Mo in one blastomere at eight cell stage leads to muscle defects at the injected side (Figure 13B). In situ hybridisation for *muscle actin* and transverse trunk sections show that Rspo2Mo injection causes disorganized somites (panels a-b) and reduced myotomes (panels c-d). Lineage tracing experiments showed that Rspo2Mo injected cells contribute to lateral plate mesoderm instead of somites or undergo cell death (data not shown). At gastrula stage expression of the myogenic markers *myf5* and *myoD* is strongly down-regulated at the Rspo2Mo injected side (panels e-h), while the pan-mesodermal marker *Xhra* and the organizer marker *Xnot2* are unaffected (panels i-i).

To test the specificity of Rspo2Mo, rescue experiments were performed by co-injecting Rspo2Mo together with a *Rspo2* RNA, in which six non-coding nucleotides were mutated so that it would not be targeted by this Morpholino. Expression of *myf5* (Figure 13C) and *myoD* (data not shown) is effectively rescued by this mutant *Rspo2* RNA, indicating that the effect of Rspo2Mo an myogenesis is specific.

Rspo2Mo was used as a tool to examine the epistatic position of *Rspo* in the Wnt/ß-catenin pathway. As read out for Wnt/ß-catenin signalling the expression of *myf5* and *muscle actin* in marginal zone explants was used (Figure 13D). In DMZ and VMZ explants, *Wnt8* DNA induces *myf5* and *muscle actin* and this induction is significantly blocked by Rspo2Mo (Figue 13D, panels a-b, lanes 3-4). However, *myf5* and *muscle actin* induction by intracellular activators of the Wnt pathway like *dishevelled, dnGSK-3ß* and *ß-catenin* is unaffected by Rspo2Mo (a-b, lanes 5-10). In LMZ explants, Rspo2Mo Injection down-

regulates endogenous *myf5* and *muscle actin* expression (Figure 13D, panels c-d, lanes 1-2). In DNA coinjections this effect is rescued effectively by ß-*catenin*- but only poorly by *XWnt8* (lanes 3-6). The residual effect of *XWnt8* is likely due to its non-cell autonomous action an cells that did not receive Rspo2Mo. Taken together these results indicate that *Rspo2* affects the Wnt/ß-catenin pathway at the level or upstream of *dishevelled*.

Example 9
R-spondins are required for Wnt/ß-catenin signalling in HeLa cells

Next the requirement of *Rspo2* for Wnt signalling was tested in mammalian cells using siRNA. Since there are four *R-spondins* with apparently redundant function, HeLa cells were selected, that only express Rspo3 and very weakly *Rspo2* (Figure 14A). Various other cell lines, such as 293T cells, express all four genes, complicating a siRNA approach.

siRNA mediated gene knock-down was carried out by transfecting pSUPER constructs (Brummelkamp et al., Science 296 (2002), 3286-3305) to produce siRNAs targeted against *Rspo2* and -3 (siRNA *Rspo 2,3*). As control, a non-sense siRNA was used. To test the efficiency of siRNA, FLAGtagged human *Rspo3* was co-transfected with siRNAs and its production was repressed by siRNA *Rspo3* but not siRNA *Rspo2* (Figure 14B).

In Wnt-reporter assays, both siRNA *Rspo2* and -3 decreased Wnt3a-induced luciferase activity compared to control siRNA (Figure 14C). When siRNA *Rspo2* and -3 are co-transfected, reporter activity drops to 40%. This effect is specific since the decreased Wnt signalling can be rescued by co-transfected mouse *Rspo2*, which is not targeted by siRNAs against human *R-*

spondins (Figure 14C). Furthermore, unlike Wnt3a-induced reporter activity, siRNA *Rspo2+3* do not affect Li$^+$-induced Wnt/ß-catenin signalling (Figure 14D). Since Li$^+$ acts by inhibiting GSK3ß activity, this is again consistent with *Rspo2* acting at the level or upstream of *dishevelled.*conclude that in HeLa cells R-spondins are required for füll Wnt/ß-catenin signalling.

Example 10
Futrin expression is deregulated in human tumors

Misregulation of Wnt/ß-catenin signalling is implicated in tumorigenesis, e.g., colon cancer, breast cancer and melanoma (Barker et al., 2000; Bienz and Clevers, 2000; Polakis, 2000). Since *R-spondins (futrins)* promote Wnt/ß-catenin signalling they may also play a role in tumorigenesis. Thus, the expression of Futrin 1-4 in various normal and cancerous human tissues was studied using radioactive hybridisation on Clontech Cancer Profiling Array II. Hybridization with ubiquitin probe was used for normalisation. The results show that expression of Futrins 1-3 is dramatically deregulated in cancerous human tissues (Figure 15). In most of the tumors the expression of Futrins 1-3 is dramatically decreased (colon, stomach, lung, rectum tumors for Futrin 1, breast, ovary, bladder, uterus, cervix, rectum tumors for Futrin 2, uterus and cervix tumors for Futrin 3). In a few cases the expression of Futrin 1-3 is upregulated (one case of stomach tumor for Futrin 1 and 2, ovary tumor for Futrin 3). Futrin 4 shows very low level of expression in most of the tissues studied, except ovary. Further results are shown in Figure 16 also showing that *HRspo1 is* weakly expressed in adult organs. It shows upregulation in ovary tumours from two patients and in one stomach tumour sample. *HRspo2* is expressed in organs of endodermal origin, including colon, rectum, small intestine and lung. Its expression decreased

in corresponding tumour samples. *HRspo3* is expressed widely and decreases in many tumour samples. In general, the expression of *hRspo1-3* is deregulated in a number of tumours, while *hRspo4* expression is very weak both in human adult organs and tumours (data not shown).